

Hayes, Robert

1817

#18

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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/484,594A

DATE: 08/18/97
TIME: 14:34:46

INPUT SET: S19735.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: O'Brien, John S.
6 Kishimoto, Yasuo
7
8 (ii) TITLE OF INVENTION: USE OF PROSAPOSIN AND NEUROTROPHIC PEPTIDES
9 DERIVED THEREFROM
10
11 (iii) NUMBER OF SEQUENCES: 11
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Knobbe, Martens, Olson and Bear
15 (B) STREET: 620 Newport Center Drive, Sixteenth Floor
16 (C) CITY: Newport Beach
17 (D) STATE: CA
18 (E) COUNTRY: USA
19 (F) ZIP: 92660
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Diskette
23 (B) COMPUTER: IBM Compatible
24 (C) OPERATING SYSTEM: DOS
25 (D) SOFTWARE: FastSEQ for Windows Version 2.0
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: 08/484,594
29 (B) FILING DATE: 07-JUN-1995
30 (C) CLASSIFICATION:
31
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: 08/100,247
34 (B) FILING DATE: 30-JUL-1993
35
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: Israelsen, Ned A
38 (B) REGISTRATION NUMBER: 29,655
39 (C) REFERENCE/DOCKET NUMBER: MYELOS.002DV2
40
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: 619-235-8550
43 (B) TELEFAX: 619-235-0176
44 (C) TELEX:
45
46

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47         (2) INFORMATION FOR SEQ ID NO:1:
48
49         (i) SEQUENCE CHARACTERISTICS:
50             (A) LENGTH: 22 amino acids
51             (B) TYPE: amino acid
52             (C) STRANDEDNESS: single
53             (D) TOPOLOGY: linear
54
55         (ii) MOLECULE TYPE: peptide
56         (v) FRAGMENT TYPE: internal
57
58         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
59
60         Cys Glu Phe Leu Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys
61         1             5             10             15
62         Thr Glu Lys Glu Ile Leu
63         20
64
65         (2) INFORMATION FOR SEQ ID NO:2:
66
67         (i) SEQUENCE CHARACTERISTICS:
68             (A) LENGTH: 523 amino acids
69             (B) TYPE: amino acid
70             (C) STRANDEDNESS: single
71             (D) TOPOLOGY: linear
72
73         (ii) MOLECULE TYPE: peptide
74         (v) FRAGMENT TYPE: N-terminal
75
76         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
77
78         Met Tyr Ala Leu Phe Leu Leu Ala Ser Leu Leu Gly Ala Ala Leu Ala
79         1             5             10             15
80         Gly Pro Val Leu Gly Leu Lys Glu Cys Thr Arg Gly Ser Ala Val Trp
81         20             25             30
82         Cys Gln Asn Val Lys Thr Ala Ser Asp Cys Gly Ala Val Lys His Cys
83         35             40             45
84         Leu Gln Thr Val Trp Asn Lys Pro Thr Val Lys Ser Leu Pro Cys Asp
85         50             55             60
86         Ile Cys Lys Asp Val Val Thr Ala Ala Gly Asp Met Leu Lys Asp Asn
87         65             70             75             80
88         Ala Thr Glu Glu Glu Ile Leu Val Tyr Leu Glu Lys Thr Cys Asp Trp
89         85             90             95
90         Leu Pro Lys Pro Asn Met Ser Ala Ser Cys Lys Glu Ile Val Asp Ser
91         100            105            110
92         Tyr Leu Pro Val Ile Leu Asp Ile Ile Lys Gly Glu Met Ser Arg Pro
93         115            120            125
94         Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Glu Ser Leu Gln Lys His
95         130            135            140
96         Leu Ala Glu Leu Asn His Gln Lys Gln Leu Glu Ser Asn Lys Ile Pro
97         145            150            155            160
98         Glu Leu Asp Met Thr Glu Val Val Ala Pro Phe Met Ala Asn Ile Pro
99         165            170            175

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100  Leu Leu Leu Tyr Pro Gln Asp Gly Pro Arg Ser Lys Pro Gln Pro Lys
101              180              185              190
102  Asp Gly Asp Val Cys Gln Asp Cys Ile Gln Met Val Thr Asp Ile Gln
103              195              200              205
104  Thr Ala Val Arg Thr Asn Ser Thr Phe Val Gln Ala Leu Val Glu His
105              210              215              220
106  Val Lys Glu Glu Cys Asp Arg Leu Gly Pro Gly Met Ala Asp Ile Cys
107              225              230              235              240
108  Lys Asn Tyr Ile Ser Gln Tyr Ser Glu Ile Ala Ile Gln Met Met Met
109              245              250              255
110  His Met Gln Pro Lys Glu Ile Cys Ala Leu Val Gly Phe Cys Asp Glu
111              260              265              270
112  Val Lys Glu Met Pro Met Gln Thr Leu Val Pro Ala Lys Val Ala Ser
113              275              280              285
114  Lys Asn Val Ile Pro Ala Leu Asp Leu Val Asp Pro Ile Lys Lys His
115              290              295              300
116  Glu Val Pro Ala Lys Ser Asp Val Tyr Cys Glu Val Cys Glu Phe Leu
117              305              310              315              320
118  Val Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu
119              325              330              335
120  Ile Leu Asp Ala Phe Asp Lys Met Cys Ser Lys Leu Pro Lys Ser Leu
121              340              345              350
122  Ser Glu Glu Cys Gln Glu Val Val Asp Thr Tyr Gly Ser Ser Ile Leu
123              355              360              365
124  Ser Ile Leu Leu Glu Glu Val Ser Pro Glu Leu Val Cys Ser Met Leu
125              370              375              380
126  His Leu Cys Ser Gly Thr Arg Leu Pro Ala Leu Thr Val His Val Thr
127              385              390              395              400
128  Gln Pro Lys Asp Gly Gly Phe Cys Glu Val Cys Lys Lys Leu Val Gly
129              405              410              415
130  Thr Leu Asp Arg Asn Leu Glu Lys Asn Ser Thr Lys Gln Glu Ile Leu
131              420              425              430
132  Ala Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp Pro Tyr Gln Lys
133              435              440              445
134  Gln Cys Asp Gln Phe Val Ala Glu Tyr Glu Pro Val Leu Ile Glu Ile
135              450              455              460
136  Leu Val Glu Val Met Asp Pro Ser Phe Val Cys Leu Lys Ile Gly Ala
137              465              470              475              480
138  Cys Pro Ser Ala His Lys Pro Leu Leu Gly Thr Glu Lys Cys Ile Trp
139              485              490              495
140  Gly Pro Ser Tyr Trp Cys Gln Asn Thr Glu Thr Ala Ala Gln Cys Asn
141              500              505              510
142  Ala Val Glu His Cys Lys Arg His Val Trp Asn
143              515              520

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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153 (ii) MOLECULE TYPE: protein
154 (v) FRAGMENT TYPE: internal
155
156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
157
158 Ser Asp Val Tyr Cys Glu Val Cys Glu Phe Leu Val Lys Glu Val Thr
159 1 5 10 15
160 Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu Ile Leu Asp Ala Phe
161 20 25 30
162 Asp Lys Met Cys Ser Lys Leu Pro Lys Ser Leu Ser Glu Glu Cys Gln
163 35 40 45
164 Glu Val Val Asp Thr Tyr Gly Ser Ser Ile Leu Ser Ile Leu Leu Glu
165 50 55 60
166 Glu Val Ser Pro Glu Leu Val Cys Ser Met Leu His Leu Cys Ser Gly
167 65 70 75 80
168

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2740 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

181	ATGTACGCC	TCTTCCTCCT	GGCCAGCCTC	CTGGGCGCGG	CTCTAGCCGG	CCCGGTCCTT	60
182	GGACTGAAAG	AATGCACCAG	GGGCTCGGCA	GTGTGGTGCC	AGAATGTGAA	GACGGCGTCC	120
183	GACTGCGGGG	CAGTGAAGCA	CTGCCTGCAG	ACCGTTTGGA	ACAAGCCAAC	AGTGAATCC	180
184	CTTCCCTGCG	ACATATGCAA	AGACGTTGTC	ACCGCAGCTG	GTGATATGCT	GAAGGACAAT	240
185	GCCACTGAGG	AGGAGATCCT	TGTTTACTTG	GAGAAGACCT	GTGACTGGCT	TCCGAAACCG	300
186	AACATGTCTG	CTTCATGCAA	GGAGATAGTG	GACTCCTACC	TCCCTGTCAT	CCTGGACATC	360
187	ATTAAAGGAG	AAATGAGCCG	TCCTGGGGAG	GTGTGCTCTG	CTCTCAACCT	CTGCGAGTCT	420
188	CTCCAGAAGC	ACCTAGCAGA	GCTGAATCAC	CAGAAGCAGC	TGGAGTCCAA	TAAGATCCCA	480
189	GAGCTGGACA	TGACTGAGGT	GGTGGCCCCC	TTCATGGCCA	ACATCCCTCT	CCTCCTCTAC	540
190	CCTCAGGACG	GCCCCCGCAG	CAAGCCCCAG	CCAAAGGATA	ATGGGGACGT	TTGCCAGGAC	600
191	TGCATTGAGA	TGGTGACTGA	CATCCAGACT	GCTGTACGGA	CCAACTCCAC	CTTTGTCCAG	660
192	GCCTTGGTGG	AACATGTCAA	GGAGGAGTGT	GACCGCCTGG	GCCCTGGCAT	GGCCGACATA	720
193	TGCAAGAACT	ATATCAGCCA	GTATTCTGAA	ATTGCTATCC	AGATGATGAT	GCACATGCAA	780
194	CCCAAGGAGA	TCTGTGCGCT	GGTTGGGTTT	TGTGATGAGG	TGAAAGAGAT	GCCCATGCAG	840
195	ACTCTGGTCC	CCGCCAAAGT	GGCCTCCAAG	AATGTCATCC	CTGCCCTGGA	ACTGGTGGAG	900
196	CCCATTAAGA	AGCAGGAGGT	CCCAGCAAAG	TCTGATGTTT	ACTGTGAGGT	GTGTGAATTC	960
197	CTGGTGAAAG	AGGTGACCAA	GCTGATTGAC	AACAACAAGA	CTGAGAAAAG	AATACTCGAC	1020
198	GCTTTTGACA	AAATGTGCTC	GAAGCTGCCG	AAGTCCCTGT	CGGAAGAGTG	CCAGGAGGTG	1080
199	GTGGACACGT	ACGGCAGCTC	CATCCTGTCC	ATCCTGCTGG	AGGAGGTCAG	CCCTGAGCTG	1140
200	GTGTGCAGCA	TGCTGCACCT	CTGCTCTGGC	ACGCGGCTGC	CTGCACTGAC	CGTTCACGTG	1200
201	ACTCAGCCAA	AGGACGGTGG	CTTCTGCGAA	GTGTGCAGGA	AGCTGGTGGG	TTATTTGGAT	1260
202	CGCAACCTGG	AGAAAAACAG	CACCAAGCAG	GAGATCCTGG	CTGCTCTTGA	GAAAGGCTGC	1320
203	AGCTTCCTGC	CAGACCCTTA	CCAGAAGCAG	TGTGATCACT	TTGTGGCAGA	GTACGAGCCC	1380
204	GTGCTGATCG	AGATCCTGGT	GGAGGTGATG	GATCCTTCCT	TCGTGTGCTT	GAAAATTGGA	1440
205	GCCTGCCCCCT	CGGCCCATAA	GCCCTTGTTG	GGAAGTGAAG	AGTGTATATG	GGGCCCCAAGC	1500

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206 TACTGGTGCC AGAACACAGA GACAGCAGCC CAGTGCAATG CTGTCGAGCA TTGCAAACGC 1560
207 CATGTGTGGA ACTAGGAGGA GGAATATTCC ATCTTGGCAG AAACCACAGC ATTGGTTTTT 1620
208 TTCTACTTGT GTGTCTGGGG GAATGAACGC ACAGATCTGT TTGACTTTGT TATAAAAATA 1680
209 GGGCTCCCCC ACCTCCCCCA TTTCTGTGTC CTTTATTGTA GCATTGCTGT CTGCAAGGGA 1740
210 GCCCCTAGCC CCTGGCAGAC ATAGCTGCTT CAGTGCCCTT TTTCTCTCTG CTAGATGGAT 1800
211 GTTGATGCAC TGGAGGTCTT TTAGCTGCC CTTGCATGGC GCCTGCTGGA GGAGGAGAGA 1860
212 GCTCTGCTGG CATGAGCCAC AGTTTCTTGA CTGGAGGCCA TCAACCCCTCT TGGTTGAGGC 1920
213 CTTGTTCTGA GCCCTGACAT GTGCTTGGGC ACTGGTGGGC CTGGGCTTCT GAGGTGGCCT 1980
214 CCTGCCCTGA TCAGGGACCC TCCCCGCTTT CCTGGGCCCTC TCAGTTGAAC AAAGCAGCAA 2040
215 AACAAAGGCA GTTTTATATG AAAGATTAGA AGCCTGGAAT AATCAGGCTT TTTAAATGAT 2100
216 GTAATTCCCA CTGTAATAGC ATAGGGATTT TGGAGCAGC TGCTGGTGGC TTGGGACATC 2160
217 AGTGGGGCCA AGGGTTCTCT GTCCCTGGTT CAACTGTGAT TTGGCTTTCC CGTGTCTTTC 2220
218 CTGGTGATGC CTTGTTTGGG GTTCTGTGGG TTTGGGTGGG AAGAGGGCAA TCTGCCTGAA 2280
219 TGTAACCTGC TAGCTCTCCG AAGGCCCTGC GGGCCTGGCT TGTGTGAGCG TGTGGACAGT 2340
220 GGTGGCCGCG CTGTGCCTGC TCGTGTGCTT TACATGTCCC TGGCTGTTGA GGCCTGCTT 2400
221 CAGCCTGCAC CCCTCCCTTG TCTCATAGAT GCTCCTTTTG ACCTTTTCAT TATAATATGG 2460
222 ATGGCGAGCT CCTAGGCCCTC TGGCTTCCTG GTAGAGGGCG GCATGCCGAA GGGTCTGCTG 2520
223 GGTGTGGATT GGATGCTGGG GTGTGGGGGT TGGGAAGCTGT CTGTGGCCCA CTTGGGCACC 2580
224 CACGCTTCTG TCCACTTCTG GTTGCCAGGA GACAGCAAGC AAAGCCAGCA GGACATGAAG 2640
225 TTGCTATTAA ATGGACTTCG TGATTTTTGT TTTGCACTAA AGTTTCTGTG ATTTAACAAT 2700
226 AAAATTCTGT TAGCCAGAAA AAAAAAAAAA AAAAAAAAAA 2740

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

241 Tyr Lys Glu Val Thr Lys Leu Ile Asp Asn Asn Lys Thr Glu Lys Glu
242 1 5 10 15
243 Ile Leu

```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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258 Cys Gln Phe Val Met Asn Lys Phe Ser Glu Leu Ile Val Asn Asn Ala

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SEQUENCE VERIFICATION REPORT
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Line

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Original Text